

In the Specification:

Please replace the first three paragraphs at page 28 with the following amended paragraphs:

Figure 1 shows *CaKRE5* sequence and comparison to the *S. cerevisiae KRE5*, *Drosophila melanogaster UGGT1*, and *S. pombe GPT1* encoded proteins. (A) illustrates nucleotide (SEQ ID NO: 1) and predicted amino acid sequence of CaKre5p (SEQ ID NO: 2). The CaKre5p signal peptide is underlined in bold. The ER retention sequence His-Asp-Glu-Leu (HDEL) is indicated in bold at the C-terminus. Non-canonical CTG codons encoding Ser in place of Leu are italicized. (B) Shows protein sequence alignment between CaKre5p, Kre5p (SEQ ID NO: 7), Gpt1p (SEQ ID NO: 9), and Uggt5p (SEQ ID NO: 8). Proteins are shown in single-letter amino acid code with amino acid identities shaded in black and similarities shaded in gray. Gaps introduced to improve alignment are indicated by dashes and amino acid positions are shown at the left;

Figure 2 shows *CaALR1* and comparison to *S. cerevisiae Alr1p* (SEQ ID NO: 10), and *S. cerevisiae Alr2p* (SEQ ID NO: 11). (A) illustrates nucleotide (SEQ ID NO: 3) and predicted amino acid sequence (SEQ ID NO: 4) of *CaALR1*. Two hydrophobic amino acid stretches predicted to serve as transmembrane domains are indicated in bold. Non-canonical CTG codons are italicized. (B) shows protein sequence alignment between CaAlr1p, Alr1p, and Alr2p. Proteins are shown in single-letter amino acid coded with amino acid identities shaded in black and similarities shaded in gray. Dashes indicate gaps introduced to improve alignment.

Figure 3 shows *CaCDC24* sequence and comparison to *CDC24* from *S. cerevisiae* and *S. pombe*. (A) illustrates nucleotide (SEQ ID NO: 5) and predicted amino acid (SEQ ID NO: 6) sequence of *CaCDC24*. Non-canonical CTG codons are italicized. (B) shows protein sequence alignment between CaCdc24p, *S. cerevisiae Cdc24p* (SEQ ID NO: 12), and the *S. pombe homolog, Scd1p* (SEQ ID NO: 13). The CaCdc24p dbl homology domain extends from amino acids 280-500. A pleckstrin homology domain is detected from residues 500-700. Protein alignments are formatted as described in Fig. 1 and 2; and

Please insert the following page, which contains the ABSTRACT of the disclosure, after page 50 of the specification as filed.